

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2002, 22:09:46 : Search time 230 Seconds  
(without alignments)  
14931.728 Million cell updates/sec

Title: US-10-025-514-7  
Perfect score: 1525  
Sequence: 1 tctagaccatctctggaag.....ccaaactcagaagtgcgac 1525

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues 4370478  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :				N_Geneseq_101002:*
1:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1980.DAT.*	
2:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1981.DAT.*	
3:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1982.DAT.*	
4:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1983.DAT.*	
5:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1984.DAT.*	
6:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1985.DAT.*	
7:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1986.DAT.*	
8:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1987.DAT.*	
9:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1988.DAT.*	
10:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1989.DAT.*	
11:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1990.DAT.*	
12:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1991.DAT.*	
13:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1992.DAT.*	
14:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1993.DAT.*	
15:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1994.DAT.*	
16:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1995.DAT.*	
17:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1996.DAT.*	
18:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1997.DAT.*	
19:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1998.DAT.*	
20:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA1999.DAT.*	
21:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA2000.DAT.*	
22:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA2001A.DAT.*	
23:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA2001B.DAT.*	
24:	/SID22/gcgdata/gene	seq/gene	seq-emb1/NA2002.DAT.*	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Match	Length	Description
1	1525	100.0	1525	24 DNA sequence encod
2	1196	78.4	1756	24 DNA sequence encod
3	1194.8	78.3	1582	24 DNA sequence encod
4	1191.6	78.1	1525	24 DNA sequence encod
5	1191.4	78.1	1582	24 DNA sequence encod
6	1191.4	78.1	1756	24 DNA sequence encod
7	1182	77.5	1182	24 DNA encoding human
8	629.4	41.3	1260	19 Codon-optimised RA
9	436.4	28.6	1312	16 Human alpha-1-try

10	436.4	28.6	1312	19	AAV28471	Nucleotide sequenc
11	436.4	28.6	1312	21	AA290199	Human alpha-anti
12	433.4	28.4	1367	22	AA345052	cDNA encoding nove
13	433.2	28.4	1352	13	AAQ31403	Human alpha-1 anti
14	433.2	28.4	1352	24	ABL67511	Thyroid cancer rel
15	433.2	28.4	1371	24	ABR84495	Human cDNA differe
16	433.2	28.4	1371	24	ABL67510	Sequence encoding
17	433.2	28.4	1433	10	AA91077	Sequence encoding
18	433.2	28.4	1434	5	AA40078	Human alpha-anti-
19	433.2	28.4	1434	20	AA83548	Nucleotide sequenc
20	433.2	28.4	5932	21	AA245928	Nucleotide sequenc
21	433.2	28.4	6142	21	AA245932	Nucleotide sequenc
22	433.2	28.4	6142	21	AA245933	Nucleotide sequenc
23	433.2	28.4	6565	21	AA245925	Nucleotide sequenc
24	433.2	28.4	6714	21	AA245930	Nucleotide sequenc
25	433.2	28.4	6924	21	AA245934	Nucleotide sequenc
26	433.2	28.4	6924	21	AA245935	Nucleotide sequenc
27	433.2	28.4	6981	21	AA245931	Nucleotide sequenc
28	433.2	28.4	7054	21	AA245927	Nucleotide sequenc
29	432.8	28.4	7405	21	AA245926	Nucleotide sequenc
30	431.6	28.3	1352	18	AA72858	Nucleotide sequenc
31	430.4	28.2	1185	19	AAV41726	Human alpha-1-anti
32	430.4	28.2	1434	10	AA90341	Native coding sequ
33	429.6	28.2	1312	10	AA97127	Sequence of alpha-
34	429.6	28.2	1189	13	AAQ21125	Alpha-1-antitrypsi
35	428.4	28.1	1378	13	AAQ23746	Alpha-1-antitrypsi
36	428.4	28.1	1396	11	AAQ03184	Entire sequence of
37	426.8	28.0	1185	7	AA60417	Human alpha 1-anti
38	426.8	28.0	1423	6	AA50425	Sequence encoding
39	425.2	27.9	1299	6	AA50540	Sequence of human
40	425.2	27.9	1378	6	AA50021	Sequence encoding
41	411.2	27.0	1390	22	AAH23089	Osteoarthritis tis
42	401.4	26.3	2013	24	ABL59152	Sequence of fusion
43	375.6	24.6	1242	18	AA79493	Protease inhibitor
44	362.8	23.8	1242	18	AA78180	Recombinant squirr
45	360.8	23.7	1312	10	AA91078	Alpha-1-antitrypsi

ALIGNMENTS

RESULT 1		
ABK88022		
ID	ABK88022 standard; DNA; 1525 BP.	
XX		
AC	ABK88022;	
XX		
DT	07-OCT-2002 (first entry)	
XX		
DE	DNA sequence encoding SLAP1 fusion protein.	
XX		
KW	Yeast; alpha factor; gene; ds; Alzheimer's disease; SLAP1;	
KW	malaria; emphysema; asthma; chronic obstructive pulmonary disease;	
KW	cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;	
KW	human immunodeficiency virus; atopic dermatitis; muscular dystrophy;	
KW	herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;	
KW	tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;	
KW	glomerulonephritis; scleroderma; hypertension.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
FF	Key	Location/Qualifiers
FT	RBS	6..8
FT		/*tag= a
FT		/standard_name= "Ribosome binding site"
FT	CDS	9..1520
FT		/*tag= b
FT		/product= "SLAP1 fusion protein"
FT		12..332
FT	misc_feature	/*tag= C
FT		/note= "SLPI coding region"
FT	misc_feature	333-335

/\*tag= d  
/note= "linking codon"  
336..1517  
/\*tag= e  
/note= "AAT coding region"

FT misc\_feature  
FT 336..1517  
FT 336..1517  
FT 336..1517  
XX WO200250287-A2.  
XX PD 27-JUN-2002.  
XX 18-DEC-2001; 2001WO-US49256.  
XX PF 18-DEC-2000; 2000US-256699P.  
XX PR 20-NOV-2001; 2001US-331966P.  
XX PR 20-NOV-2001; 2001US-331966P.  
XX XX (ARRI-) ARRIYA PHARM INC.  
XX PA  
XX XX  
XX PI Barr PJ, Gibson HL, Pemberton P;  
XX WPI; 2002-500631/53.  
XX DR P-PSDB; AAU99881.  
XX DR

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Example 1; Page 73-73; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the SLAP1 fusion protein of the invention.

Sequence 1525 BP; 467 A; 286 C; 314 G; 458 T; 0 other;

Query Match 100.0%; Score 1525; DB 24; Length 1525;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGACCATGCTCGAAGTCTTTCAAGCGCGGTGTTTGTCACCAAGAGTCCGCTC 60  
DB 1 TCTAGACCATGCTCGAAGTCTTTCAAGCGCGGTGTTTGTCACCAAGAGTCCGCTC 60  
QY 61 AATGTTTGAGATACAGAGACGAGATGTCATCCGATGCGCAATGTCAGGTAGAAGA 120  
DB 61 AATGTTTGAGATACAGAGACGAGATGTCATCCGATGCGCAATGTCAGGTAGAAGA 120  
QY 121 GATGTTGTCACAGACACTTGGGTATCAAGTGTCTAGACCCAGTTCACACCCCAACCCAA 180  
DB 121 GATGTTGTCACAGACACTTGGGTATCAAGTGTCTAGACCCAGTTCACACCCCAACCCAA 180  
QY 181 CTAGAGAAAGCCAGGTAAGTGTCCAGTTACTTACGGTCAATGTTGATGTGAACCCAC 240  
DB 181 CTAGAGAAAGCCAGGTAAGTGTCCAGTTACTTACGGTCAATGTTGATGTGAACCCAC 240  
QY 241 CAACACTTCTGTAATGGACGGTCAATGTAAGAGACACTTGAAGTGTGTTGATGGGTATGT 300  
DB 241 CAACACTTCTGTAATGGACGGTCAATGTAAGAGACACTTGAAGTGTGTTGATGGGTATGT 300

QY 1381 GCCTATGTTCTGGAAGCTATTCCATGAGCATTCACAGAGCTTAATTAATAAC 1440  
 |||||||  
 Db 1381 GCCTATGTTCTGGAAGCTATTCCATGAGCATTCACAGAGCTTAATTAATAAC 1440  
 |||||||  
 QY 1441 CATTCTGTTTCTGATGATCGAGCAGACACTAAAGGCCATTGTTATGGGTAAGGTTG 1500  
 |||||||  
 Db 1441 CATTCTGTTTCTGATGATCGAGCAGACACTAAAGGCCATTGTTATGGGTAAGGTTG 1500  
 |||||||  
 QY 1501 TCAACCCAACTCAGAGTAGTCGAC 1525  
 |||||||  
 Db 1501 TCAACCCAACTCAGAGTAGTCGAC 1525  
 |||||||

## RESULT 2

ABK88023

ID ABK88023 standard; DNA; 1756 BP.

XX AC ABK88023;

DT 07-OCT-2002 (first entry)

XX DE DNA sequence encoding TAP1 fusion protein.

XX KW TAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;  
 KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
 KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;  
 KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
 KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
 KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
 KW glomerulonephritis; hypertension.

XX OS Homo sapiens.

OS Synthetic.

XX FH Key

Location/Qualifiers

FT RBS 6..8

FT /\*tag= a

FT /standard\_name= "Ribosome binding site"

FT 9..1751

FT /\*tag= b

FT /product= "TAP1 fusion protein"

FT 12..563

FT /\*tag= c

FT /note= "TIMP-1 coding region"

FT 564..566

FT /\*tag= d

FT /note= "linking codon"

FT 567..1748

FT /\*tag= e

FT /note= "AAT coding region"

XX PN WO200250287-A2.

XX XX 27-JUN-2002.

XX XX 18-DEC-2001; 2001WO-US49256.

XX XX 18-DEC-2000; 2000US-256699P.

XX XX 20-NOV-2001; 2001US-331966P.

XX XX (ARRI-) ARRIVA PHARM INC.

XX XX Barr PJ, Gibson HL, Pemberton P;

XX XX WPI; 2002-500631/53.

XX XX P-PSDB; AAU99882.

XX PT Novel fusion protein useful for inhibiting protease activity associated  
 XX with a disorder such as emphysema, asthma, comprises a first protease  
 XX inhibitor comprising alpha 1-antitrypsin and a second protease  
 XX inhibitor

PS

XX

Example 1; Page 77-78; 134pp; English.

CC This invention relates to a novel fusion protein comprising a first  
 CC protease inhibitor comprising an alpha-antitrypsin or its functionally  
 CC active portion and a second protease inhibitor or its functionally  
 CC active protein. The fusion proteins of the invention may act as an  
 CC inhibitor of protease activity. The fusion protein of the invention  
 CC is useful for inhibiting protease activity associated with a disorder  
 CC such as emphysema, asthma, chronic obstructive pulmonary disease,  
 CC cystic fibrosis, otitis media, otitis externa or HIV infection, or  
 CC for treating an individual suffering from or at risk for a disease or  
 CC disorder involving unwanted protease activity. The proteins are useful  
 CC for treating dermatological diseases such as atopic dermatitis, eczema  
 CC and psoriasis, in inflammatory responses to viral infection, and for  
 CC treating herpes infection, corneal or epidermal ulceration, chronic  
 CC non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,  
 CC tumour metastasis and tumour angiogenesis, gastric ulceration,  
 CC osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,  
 CC bacterial infection, Alzheimer's disease, hypertension and muscular  
 CC dystrophy. The present sequence represents the DNA encoding the  
 CC TAP1 fusion protein of the invention.

XX SQ Sequence 1756 BP; 493 A; 395 C; 373 G; 495 T; 0 other;

## Query Match

78.4%; Score 1196; DB 24; Length 1756;

Best Local Similarity 100.0%; Pred. No. 1.4e-290;

Matches 1196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 330 GCCATGGAAGACCCCTCAAGCGCAGCGCGCTCAAAAAACCGACACCATCATCAGACCAA 389

|||||

Db 561 GCCATGGAAGACCCCTCAAGCGCAGCGCGCTCAAAAAACCGACACCATCATCAGACCAA 620

|||||

QY 390 GACCATCCGACTTTTAAATAAAATTAATCTCAAAATTTAGCCGAATTTCTTTCTTTGTAT 449

|||||

Db 621 GACCATCCGACTTTTAAATAAAATTAATCTCAAAATTTAGCCGAATTTCTTTCTTTGTAT 680

|||||

QY 450 AGACAATTAGCTCATCAAGTAATTTCTACTAATCAATTTTATAGTCTCTGTTCTATTGCC 509

|||||

Db 681 AGACAATTAGCTCATCAAGTAATTTCTACTAATCAATTTTATAGTCTCTGTTCTATTGCC 740

|||||

QY 510 ACTGCTTTCGCCATGTTAGTTTGTAGTACTAAAGCCGATACCCATGACGAGATTTTAGAA 569

|||||

Db 741 ACTGCTTTCGCCATGTTAGTTTGTAGTACTAAAGCCGATACCCATGACGAGATTTTAGAA 800

|||||

QY 570 GGTAAACTTTAAATTTGACCGAAATCCAGAGCCCAATTCACGAGGTTTTCAGAG 629

|||||

Db 801 GGTAAACTTTAAATTTGACCGAAATCCAGAGCCCAATTCACGAGGTTTTCAGAG 860

|||||

QY 630 TTGTTGAGAACTTTGAATCAACCTGATTCTCAATTTGCAATTAATTAATTAATTAATTAAT 689

|||||

Db 861 TTGTTGAGAACTTTGAATCAACCTGATTCTCAATTTGCAATTAATTAATTAATTAATTAAT 920

|||||

QY 690 TTTTCTGCTGAGGTTTAAATTTGTTGACAAATTCCTAGAGAGCGTCAAGAACTATAT 749

|||||

Db 921 TTTTCTGCTGAGGTTTAAATTTGTTGACAAATTCCTAGAGAGCGTCAAGAACTATAT 980

|||||

QY 750 CATAGTGAGGCTTTTACCGTTAAATTTGCTGATCTACTGAGAGAGCTTAAAGAACTAAT 809

|||||

Db 981 CATAGTGAGGCTTTTACCGTTAAATTTGCTGATCTACTGAGAGAGCTTAAAGAACTAAT 1040

|||||

QY 810 GATTATGTTGAGAAAGGCCACCCAGGTTAAGATCGTTGACCTAGTTTAAAGAACTAGATCGT 869

|||||

Db 1041 GATTATGTTGAGAAAGGCCACCCAGGTTAAGATCGTTGACCTAGTTTAAAGAACTAGATCGT 1100

|||||

QY 870 GATACCGTCTTCGCACTAGTTTAACTATATATTTTCAAGGGTAAAGTGGGAACGCTCCTTTC 929

|||||

Db 1101 GATACCGTCTTCGCACTAGTTTAACTATATATTTTCAAGGGTAAAGTGGGAACGCTCCTTTC 1160

|||||

QY 930 GAGGTTAAAGATACAGAGAGCAATTTTCATGTTGATCAAGTTACTACTGTCAGAGTT 989

|||||

Db 1161 GAGGTTAAAGATACAGAGAGCAATTTTCATGTTGATCAAGTTACTACTGTCAGAGTT 1220

|||||

QY 990 CCAATGATGAAAGAGACTGGGTATGTTCAATATTCACATTTGCAAAATTAAGTCTTCTGG 1049

|||||

Mon Dec 9 12:50:50 2002

us-10-025-514-7.rng

```
Db 1221 CCAATGATGAAGACGCGGTATGCTCAATATTCACATTCGAAAAATTAAGTCTCTGG 1280
QY 1050 GTCATTATTAAGAGTATTAGGTAAGCGTACTGCTATTTTACAGACGAAGGT 1109
Db 1281 GTCATTATTAAGAGTATTAGGTAAGCGTACTGCTATTTTACAGACGAAGGT 1340
QY 1110 AAGCTTCAACATTTAGAGAATGAGTTCGACTCATGACATTAATTAAGTATTTAGAGAAC 1169
Db 1341 AAGCTTCAACATTTAGAGAATGAGTTCGACTCATGACATTAATTAAGTATTTAGAGAAC 1400
QY 1170 GAGGATCGCTAGCGCTCTCTGACCTGCCAAGTTAACTATCACCCTGCTACTGAC 1229
Db 1401 GAGGATCGCTAGCGCTCTCTGACCTGCCAAGTTAACTATCACCCTGCTACTGAC 1460
QY 1230 TTAATACTGTTTATAGGCGCAGTATAGTATTAACCAAGTTTCTTAAACGCTGCGGATTTG 1289
Db 1461 TTAATACTGTTTATAGGCGCAGTATAGTATTAACCAAGTTTCTTAAACGCTGCGGATTTG 1520
QY 1290 AGTGTGTTACTGAAGAAGTCCATTAATAATGAGTAAAGCTGTTCAAGAGCGGCTCTTA 1349
Db 1521 AGTGTGTTACTGAAGAAGTCCATTAATAATGAGTAAAGCTGTTCAAGAGCGGCTCTTA 1580
QY 1350 ACTATTGATGAAGAGGTAACGAGCGCGCGCTATGTTCTTGAAGCTATTTCCCAATG 1409
Db 1581 ACTATTGATGAAGAGGTAACGAGCGCGCGCTATGTTCTTGAAGCTATTTCCCAATG 1640
QY 1410 ASCATTCCACCAGAAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGACGAGAAC 1469
Db 1641 ASCATTCCACCAGAAAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGACGAGAAC 1700
QY 1470 ACTAAAGCCGATGTTTATGGTGAAGTGTGCAACCAACTCAGAACTAGTCGAC 1525
Db 1701 ACTAAAGCCGATGTTTATGGTGAAGTGTGCAACCAACTCAGAACTAGTCGAC 1756

RESULT 3
ABK88024
ID ABK88024 standard; DNA; 1582 BP.
AC AC
XX ABK88024;
XX
XX
XX
XX 07-OCT-2002 (first entry)
XX
XX DNA sequence encoding N-TAP1 fusion protein.
XX
XX NTAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;
KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;
KW glomerulonephritis; hypertension.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
XX
XX Key Location/Qualifiers
XX RBS 6..8
XX /tag= a
XX /standard_name= "Ribosome binding site"
XX CDS 9..1577
XX /tag= b
XX /product= "NTAP1 fusion protein"
XX 12..389
XX misc_feature
XX /tag= c
XX /note= "TIMP-1 coding region"
XX 390..392
XX misc_feature
XX /tag= d
XX /note= "linking codon"
XX 393..1574
XX misc_feature
XX /tag= e
XX /note= "AAT coding region"
XX FT
```

```
XX WO200250287-A2.
PN
XX 27-JUN-2002.
XX
XX 18-DEC-2001; 2001WO-US49256.
XX
XX 18-DEC-2000; 2000US-256699P.
XX
XX 20-NOV-2001; 2001US-331966P.
XX
XX (ARRI-) ARRIVA PHARM INC.
XX
XX Barr PJ, Gibson HL, Pemberton P;
XX
XX WPI: 2002-500631/53.
XX
XX P-PSDB; AAU99883.
XX
XX Novel fusion protein useful for inhibiting protease activity associated
XX with a disorder such as emphysema, asthma, comprises a first protease
XX inhibitor comprising alpha 1-antitrypsin and a second protease
XX inhibitor -
XX
XX Example 2; Page 85-86; 134pp; English.
XX
XX This invention relates to a novel fusion protein comprising a first
XX protease inhibitor comprising an alpha1-antitrypsin or its functionally
XX active portion and a second protease inhibitor or its functionally
XX active portion. The fusion proteins of the invention may act as an
XX inhibitor of protease activity. The fusion protein of the invention
XX is useful for inhibiting protease activity associated with a disorder
XX such as emphysema, asthma, chronic obstructive pulmonary disease,
XX cystic fibrosis, otitis media, otitis externa or HIV infection, or
XX for treating an individual suffering from or at risk for a disease or
XX disorder involving unwanted protease activity. The proteins are useful
XX for treating dermatological diseases such as atopic dermatitis, eczema
XX and psoriasis, in inflammatory responses to viral infection, and for
XX treating herpes infection, corneal or epidermal ulceration, chronic
XX non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,
XX tumour metastasis and tumour angiogenesis, gastric ulceration,
XX osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,
XX bacterial infection, Alzheimer's disease, hypertension and muscular
XX dystrophy. The present sequence represents the DNA encoding the
XX NTAP1 fusion protein of the invention.
XX
XX Sequence 1582 BP; 464 A; 333 C; 329 G; 456 T; 0 other;
XX
XX Query Match 78.3%; Score 1194.8; DB 24; Length 1582;
XX Best Local Similarity 99.8%; Pred. No. 2.7e-290;
XX Matches 1196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 328 AGGCCATGGAGAGCCCTCAAGCGACGCGCTCAAAAACCGACACGATCATCAGCAC 387
Db 385 AGGAATGGAGAGCCCTCAAGCGACGCGCTCAAAAACCGACACGATCATCAGCAC 444
QY 388 AAGACATCCGACCTTTAATAAATAATCTCAAAATTTAGCGAATTTGCTTTCTTGT 447
Db 445 AAGACATCCGACCTTTAATAAATAATCTCAAAATTTAGCGAATTTGCTTTCTTGT 504
QY 448 ATAGACAATTTAGCTCATCAAGTAACTTCTACTTAACATTTTCTGCTTCTATTG 507
Db 505 ATAGACAATTTAGCTCATCAAGTAACTTCTACTTAACATTTTCTGCTTCTATTG 564
QY 508 CCACCTGCTTTGCGCATGTTGAGTTTAGTACTAAAGCGCATACCATGACGAGATTTAG 567
Db 565 CCACCTGCTTTGCGCATGTTGAGTTTAGTACTAAAGCGCATACCATGACGAGATTTAG 624
QY 568 AAGGTTTAACTTTAATTTGACCGGAAATCCAGAGAGCCCAATTCACGAGGTTTCAAG 627
Db 625 AAGGTTTAACTTTAATTTGACCGGAAATCCAGAGAGCCCAATTCACGAGGTTTCAAG 684
QY 628 ACTTGTGAGAACTTTGAATCAACCTGATTTCTCAATTTCAATTAATACTACTGTAACGTT 687
Db 685 AGTTGTGAGAACTTTGAATCAACCTGATTTCTCAATTTCAATTAATACTACTGTAACGTT 744
```

```
QY 688 TATTTTCTCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCGTCAAGAACTAT 747
   |||||||
Db 745 TATTTTCTCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCGTCAAGAACTAT 804
   |||||||
QY 748 ATCATGTGAGGCTTTTACCGTTAAATTTTGGTGATCTGAGGAGCTAAAAAGCAATTA 807
   |||||||
Db 805 ATCATGTGAGGCTTTTACCGTTAAATTTTGGTGATCTGAGGAGCTAAAAAGCAATTA 864
   |||||||
QY 808 ATGATTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTAAAGAAATTTAGATC 867
   |||||||
Db 865 ATGATTATGTTGAGAAAGGACCCAGGTAAGATCGTTGACCTAGTAAAGAAATTTAGATC 924
   |||||||
QY 868 GTGATACCGCTTCGCACTAGTTAACTATATTTTTTTCAAGGGTAAGTGGGAACGTCCTT 927
   |||||||
Db 925 GTGATACCGCTTCGCACTAGTTAACTATATTTTTTTCAAGGGTAAGTGGGAACGTCCTT 984
   |||||||
QY 928 TCGAGGTTAAAGTACTGAGAGAGAGATTTTTCATGTTGATCAAGTTACTACTGTCAGAG 987
   |||||||
Db 985 TCGAGGTTAAAGTACTGAGAGAGAGATTTTTCATGTTGATCAAGTTACTACTGTCAGAG 1044
   |||||||
QY 988 TTCCAATGATGAAAGACTGGGTATGTTCAATATTCACCAATTCGAAAAATTAAGTTCCT 1047
   |||||||
Db 1045 TTCCAATGATGAAAGACTGGGTATGTTCAATATTCACCAATTCGAAAAATTAAGTTCCT 1104
   |||||||
QY 1048 GGGTCTTATTAATCAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAAG 1107
   |||||||
Db 1105 GGGTCTTATTAATCAAGTATTTAGGTAACGCTACTGCTATTTTTTTTACCAGACGAAG 1164
   |||||||
QY 1108 GTAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATTAATTAATTTTATAGAGA 1167
   |||||||
Db 1165 GTAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATTAATTAATTTTATAGAGA 1224
   |||||||
QY 1168 ACAGGATCGTCGTAGCGCTTCTCGACCTGCGCAAGTTAAGTATCACCGGTACTTAGC 1227
   |||||||
Db 1225 ACAGGATCGTCGTAGCGCTTCTCGACCTGCGCAAGTTAAGTATCACCGGTACTTAGC 1284
   |||||||
QY 1228 ACTTAAATCTGTTTATGAGCCAGTTAGGTATTAACCAAGTTTCTTCAACGGTGCGGATT 1287
   |||||||
Db 1285 ACTTAAATCTGTTTATGAGCCAGTTAGGTATTAACCAAGTTTCTTCAACGGTGCGGATT 1344
   |||||||
QY 1288 TGAGTGGTGTACTGAGAGAGTCCATTAAATTTAGTAAAGCTGTTCAAGCGGTCT 1347
   |||||||
Db 1345 TGAGTGGTGTACTGAGAGAGTCCATTAAATTTAGTAAAGCTGTTCAAGCGGTCT 1404
   |||||||
QY 1348 TAACTATTGATGAAAGGTTACCGAGCGCGCGGCTATGTTCTTGGAGCTATTCCAA 1407
   |||||||
Db 1405 TAACTATTGATGAAAGGTTACCGAGCGCGCGGCTATGTTCTTGGAGCTATTCCAA 1464
   |||||||
QY 1408 TGAGCATTCACAGAGAGTTAAATTTAATAAACCAATTCGTTTTCTGTATGATCGAGCAGA 1467
   |||||||
Db 1465 TGAGCATTCACAGAGAGTTAAATTTAATAAACCAATTCGTTTTCTGTATGATCGAGCAGA 1524
   |||||||
QY 1468 ACACTAAAAGCCCATGTTTATGGTTAGGTTGTCAACCCAACTCAGAGTAGTCGAC 1525
   |||||||
Db 1525 ACACTAAAAGCCCATGTTTATGGTTAGGTTGTCAACCCAACTCAGAGTAGTCGAC 1582
   |||||||
```

## RESULT 4

ABK88025

ID ABK88025 standard; DNA; 1525 BP.

XX AC ABK88025;

XX AC ABK88025;

XX DT 07-OCT-2002 (first entry)

XX DE DNA sequence encoding rSLAP1 fusion protein.

XX rSLAP1; gene; ds; Alzheimer's disease; tumour angiogenesis;

KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;

KW cystic fibrosis; otitis media; otitis externa; HIV; psoriasis; eczema;

KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;

KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;

KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
glomerulonephritis; hypertension.

OS Homo sapiens.  
Synthetic.

XX Key Location/Qualifiers  
RBS 6..8

FT /\*tag= a  
/\*standard\_name= "Ribosome binding site"  
9..1520

FT /\*tag= b  
/\*product= "rSLAP1 fusion protein"  
12..1193

FT /\*tag= c  
/\*note= "AAT coding region"  
1194..1196

FT /\*tag= d  
/\*note= "linking codon"  
1197..1517

FT /\*tag= e  
/\*note= "SupI coding region"  
WO200250287-A2.

XX 27-JUN-2002.

XX 18-DEC-2001; 2001WO-US49256.

XX 18-DEC-2000; 2000US-256699P.

XX 20-NOV-2001; 2001US-331966P.

XX (ARRI-) ARRIVA PHARM INC.

XX Barr PJ, Gibson HL, Pemberton P;

XX WPI: 2002-500631/53.

XX P-PSDB; RAU99884.

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Example 3; Page 89-90; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis externa or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rSLAP1 fusion protein of the invention.

Sequence 1525 BP; 467 A; 287 C; 314 G; 457 T; 0 other;

## Query Match

Best Local Similarity 78.1%; Score 1191.6; DB 24; Length 1525;

Matches 1194; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 325 TCAAGGCCATGGAAGACCCCTCAAGGCGAGCGCGCTCAAAAAACCGACACCATCATCAGC 384



is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the rN-TAP1 fusion protein of the invention.

xx  
SQ Sequence 1582 BP; 464 A; 334 C; 329 G; 455 T; 0 other;

Query Match 78.1%; Score 1191.4; DB 24; Length 1582;  
Best Local Similarity 99.5%; Pred. No. 1.9e-289;  
Matches 1195; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 325 TCAAGGCGATGGAAGACCCCTCAAGGCGACGCGCTCAAAAACCGACACAGTCATCACG 384  
DB 1 TCTAGACCATGGAGACCCCTCAAGGCGACGCGCTCAAAAACCGACACAGTCATCACG 60  
QY 385 ACCAAGACCATCCGACTTTTAAATAAATACTCCAAATTTAGCCGAATTTGCTTTTCTT 444  
DB 61 ACCAAGACCATCCGACTTTTAAATAAATACTCCAAATTTAGCCGAATTTGCTTTTCTT 120  
QY 445 TGTATAGACAAATAGTCATCAAGTAATTTCTACTACATTTTATAGTCCTGTTTCTA 504  
DB 121 TGTATAGACAAATAGTCATCAAGTAATTTCTACTACATTTTATAGTCCTGTTTCTA 180  
QY 505 TTGCCACTGCTTTTCGCGATGTTAGGTACTAAAGCGGATACCCGATGACGAGATTT 564  
DB 181 TTGCCACTGCTTTTCGCGATGTTAGGTACTAAAGCGGATACCCGATGACGAGATTT 240  
QY 565 TAGAAGGTTTAACTTTAATTTGACCGAAATCCAGAAAGCCCAAAATTCACGAGGTTTTC 624  
DB 241 TAGAAGGTTTAACTTTAATTTGACCGAAATCCAGAAAGCCCAAAATTCACGAGGTTTTC 300  
QY 625 AAGAGTTGTTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTAAGTCTGTAAGC 684  
DB 301 AAGAGTTGTTGAGAACTTTGAATCAACCTGATCTCAATTTGCAATTAAGTCTGTAAGC 360  
QY 685 GTTATTTTGTGTAAGGTTTAAATTTGTTGACAAATTTCTAGAAAGACGTCACAGAAAC 744  
DB 361 GTTATTTTGTGTAAGGTTTAAATTTGTTGACAAATTTCTAGAAAGACGTCACAGAAAC 420  
QY 745 TATATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATAGTACGAGGAGCTAAAAAGCAA 804  
DB 421 TATATCATAGTGAGGCTTTTACCGTTAATTTTGGTGATAGTACGAGGAGCTAAAAAGCAA 480  
QY 805 TTAATGATTATGTTGAGAAGCCACCGAGGTAAAGTCTGACCTAGTCTTAAGAAATTAG 864  
DB 481 TTAATGATTATGTTGAGAAGCCACCGAGGTAAAGTCTGACCTAGTCTTAAGAAATTAG 540  
QY 865 ATCGTGATACCGCTTTCGCACATAGTAACTATATTTTTCAGGGGTAAAGTGGGAACGTC 924  
DB 541 ATCGTGATACCGCTTTCGCACATAGTAACTATATTTTTCAGGGGTAAAGTGGGAACGTC 600  
QY 925 CTTTCGAGGTTAAAGATCTGAAGAGGAGATTTTCATGTTGATCAAGTACTACTGTCGA 984  
DB 601 CTTTCGAGGTTAAAGATCTGAAGAGGAGATTTTCATGTTGATCAAGTACTACTGTCGA 660  
QY 985 AAGTTCCATGATGAAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAAAATTAAGTT 1044  
DB 661 AAGTTCCATGATGAAAAGACTGGGTATGTTCAATATTTCAACATTTGCAAAAAATTAAGTT 720  
QY 1045 CTTGGGCTCTTATATGAAGTATTTAGGTAAAGTCTGCTATTTTATTTTACCAGACG 1104  
DB 721 CTTGGGCTCTTATATGAAGTATTTAGGTAAAGTCTGCTATTTTATTTTACCAGACG 780

QY 1105 AAGGTAAGCTTCAACATTTTAGAAGATGAGTTGACTCATGACATTAATACTAAATTTTAG 1164  
DB 781 AAGGTAAGCTTCAACATTTTAGAAGATGAGTTGACTCATGACATTAATACTAAATTTTAG 840  
QY 1165 AGAACGAGGATGCTGCTAGCGCTTCTCTGACCTGCGCAAGTTAAGTATCACCGGTACTT 1224  
DB 841 AGAACGAGGATGCTGCTAGCGCTTCTCTGACCTGCGCAAGTTAAGTATCACCGGTACTT 900  
QY 1225 AGACTTAAATCTGTTTTAGGCCAGTATTAGCCAAAGTTTCTTAAACGGTGGCG 1284  
DB 901 AGACTTAAATCTGTTTTAGGCCAGTATTAGCCAAAGTTTCTTAAACGGTGGCG 960  
QY 1285 ATTTGAGTGGTGTACTGGAAGAGTCCCAATTAATTAAGTAAAGCTGTTCAAAAGCG 1344  
DB 961 ATTTGAGTGGTGTACTGGAAGAGTCCCAATTAATTAAGTAAAGCTGTTCAAAAGCG 1020  
QY 1345 TCTTAACATTTGATGAAAAGGTTACCGAGCGCGCGGCTATGTTCTCGGAAGCTATTTC 1404  
DB 1021 TCTTAACATTTGATGAAAAGGTTACCGAGCGCGCGGCTATGTTCTCGGAAGCTATTTC 1080  
QY 1405 CAATGAGCATTCACACAGAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGC 1464  
DB 1081 CAATGAGCATTCACACAGAGTTAAATTTAATAAACCATTCGTTTTCTGATGATCGAGC 1140  
QY 1465 AGAACACTAAAAGCCCATTTGTTATGGTAAAGTTGTCACCCAACTCAGAAGTATGTCGA 1524  
DB 1141 AGAACACTAAAAGCCCATTTGTTATGGTAAAGTTGTCACCCAACTCAGAAGTATGTCGA 1200  
QY 1525 C 1525  
DB 1201 C 1201  
RESULT 6  
ABK88026  
ID ABK88026 standard; DNA; 1756 BP.  
XX  
AC ABK88026;  
XX  
DT 07-OCT-2002 (first entry)  
XX  
DE DNA sequence encoding rTAP1 fusion protein.  
KW rTAP1; gene: ds; Alzheimer's disease; tumour angiogenesis;  
KW malaria; emphysema; asthma; chronic obstructive pulmonary disease;  
KW cystic fibrosis; otitis media; otitis external; HIV; psoriasis; eczema;  
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;  
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;  
KW tumour metastasis; osteoporosis; Paget's disease; scleroderma;  
KW glomerulonephritis; hypertension.  
OS Homo sapiens.  
OS Synthetic.  
FH Key Location/Qualifiers  
FT RBS 6..8  
FT /\*tag= a  
FT /standard\_name= "Ribosome binding site"  
FT 9..1751  
FT /\*tag= b  
FT /product= "rTAP1 fusion protein"  
FT 12..1193  
FT /\*tag= c  
FT /note= "AT coding region"  
FT 1194..1196  
FT /\*tag= d  
FT /note= "linking codon"  
FT 1197..1748  
FT /\*tag= e  
FT /note= "TIMP-1 coding region"  
PN WO200250287-A2.  
XX

PD	27-JUN-2002.	Db	361	GTATTATTTTCTGAGGTTTAAATTTGGTTGACAAATTCCTAGAGAGCTCAAGAAAC	420
XX		Qy	745	TATATCATAGTGAGGCTTTTACCGTTTAAATTTGCTGATGACTGAGGAAGCTAAAAAGCAAA	804
PF	18-DEC-2001; 2001WO-US49256.	Db	421	TATATCATAGTGAGGCTTTTACCGTTTAAATTTGCTGATGACTGAGGAAGCTAAAAAGCAAA	480
PR	18-DEC-2000; 2000US-256699P.	Qy	805	TAATGATTATGTTGAGAAAGGCCACCCAGGGAAGATGCTGTTGACCTAGTTAAAGAAATAG	864
PR	20-NOV-2001; 2001US-331966P.	Db	481	TAATGATTATGTTGAGAAAGGCCACCCAGGGAAGATGCTGTTGACCTAGTTAAAGAAATAG	540
XX	(ARRI-) ARRIVA PHARM INC.	Qy	865	ATCGTGATACCGTCTTCGCACCTAGTTAACTATATTTTTTCAAGGTAAGTGGGAAGCTC	924
XX	Barr PJ, Gibson HL, Pemberton P;	Db	541	ATCGTGATACCGTCTTCGCACCTAGTTAACTATATTTTTTCAAGGTAAGTGGGAAGCTC	600
XX	WPI; 2002-500631/53.	Qy	925	CTTTCCGAGTTAAACATACCTGAAGAGGAGATTTTCATGTTGATCAAGTCTACTACTGTCA	984
XX	P-PSDB; AAU99889.	Db	601	CTTTCCGAGTTAAACATACCTGAAGAGGAGATTTTCATGTTGATCAAGTCTACTACTGTCA	660
PT	Novel fusion protein useful for inhibiting protease activity associated	Qy	985	AAAGTTCCAAATGATGAAAGAGCTGGGTATGTTCAATATTTCAACATTTGCAAAAATTAAGTT	1044
PT	with a disorder such as emphysema, asthma, comprises a first protease	Db	661	AAAGTTCCAAATGATGAAAGAGCTGGGTATGTTCAATATTTCAACATTTGCAAAAATTAAGTT	720
PT	inhibitor comprising alpha 1-antitrypsin and a second protease	Qy	1045	CTTTGGGCTCTTATTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTTTTTTACCAGAGC	1104
PT	inhibitor -	Db	721	CTTTGGGCTCTTATTAATGAAGTATTTAGGTAAAGCTACTGCTATTTTTTTTTTACCAGAGC	780
XX	Example 3; Page 92-93; 134pp; English.	Qy	1105	AAAGTAAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATTAATTAATTTTATAG	1164
XX	This invention relates to a novel fusion protein comprising a first	Db	781	AAAGTAAAGCTTCAACATTTAGAGATGAGTTGACTCATGACATTAATTAATTTTATAG	840
XX	protease inhibitor comprising an alpha1-antitrypsin or its functionally	Qy	1165	AGAAGAGGATCGTGTAGCCGCTTCTGACCTGCCAAGTTAAGTATACCCGCTACTT	1224
XX	active portion and a second protease inhibitor or its functionally	Db	841	AGAAGAGGATCGTGTAGCCGCTTCTGACCTGCCAAGTTAAGTATACCCGCTACTT	900
XX	active protein. The fusion proteins of the invention may act as an	Qy	1225	AGGACTTAAATCTGTTTATGAGGCTAGTTAGGTATTAACCAAGTCTTTTCTTAACGGTGGC	1284
XX	inhibitor of protease activity. The fusion protein of the invention	Db	901	AGGACTTAAATCTGTTTATGAGGCTAGTTAGGTATTAACCAAGTCTTTTCTTAACGGTGGC	960
XX	is useful for inhibiting protease activity associated with a disorder	Qy	1285	ATTGAGTGGTGTACTGTAAGAGCTCCATTAATTAATTAAGTAAAGCTGTTTCAAGAGCGG	1344
XX	such as emphysema, asthma, chronic obstructive pulmonary disease,	Db	961	ATTGAGTGGTGTACTGTAAGAGCTCCATTAATTAATTAAGTAAAGCTGTTTCAAGAGCGG	1020
XX	cystic fibrosis, otitis media, otitis externa or HIV infection, or	Qy	1345	TCTTAATCTATGATGAAAGGGTACCGAGCGCGGCTATGTTCTCTGGAAGCTATTC	1404
XX	for treating an individual suffering from or at risk for a disease or	Db	1021	TCTTAATCTATGATGAAAGGGTACCGAGCGCGGCTATGTTCTCTGGAAGCTATTC	1080
XX	tumour metastasis and tumour angiogenesis, gastric ulceration,	Qy	1405	CAATGAGCATTCACCCAGAGTTAAATTTAATAAACCATTCGTTTCTGTGATGATCGAGC	1464
XX	disorder involving unwanted protease activity. The proteins are useful	Db	1081	CAATGAGCATTCACCCAGAGTTAAATTTAATAAACCATTCGTTTCTGTGATGATCGAGC	1140
XX	for treating dermatological diseases such as atopic dermatitis, eczema	Qy	1465	AGAACACTAAAGCCCATTTGTTATGGGTAAGGTTCTCAACCCCACTCAGAAAGTAGTGA	1524
XX	and psoriasis, in inflammatory responses to viral infection, and for	Db	1141	AGAACACTAAAGCCCATTTGTTATGGGTAAGGTTCTCAACCCCACTCAGAAAGTAGTGA	1200
XX	treating herpes infection, corneal or epidermal ulceration, chronic	Qy	1525	C 1525	
XX	non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease,	Db	1201	C 1201	
XX	osteoporosis, Paget's disease, glomerulonephritis, scleroderma, malaria,	Qy	1201	C 1201	
XX	bacterial infection, Alzheimer's disease, hypertension and muscular	Db	1201	C 1201	
XX	dystrophy. The present sequence represents the DNA encoding the	Qy	1201	C 1201	
XX	rTAP1 fusion protein of the invention.	Db	1201	C 1201	
XX	Sequence 1756 BP; 493 A; 394 C; 374 G; 495 T; 0 other;	Qy	1201	C 1201	
XX	Query Match	Db	1201	C 1201	
XX	Best Local Similarity 78.1%; Score 1191.4; DB 24; Length 1756;	Qy	1201	C 1201	
XX	Matches 1195; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	Db	1201	C 1201	
Qy	325 TCAAGGCCATGGAAGACCTCAAGGCGACGCCGCTCAAAAACCGACACGATCATCAGC	384			
Db	1 TCTAGACCATGGAAGACCTCAAGGCGACGCCGCTCAAAAACCGACACGATCATCAGC	60			
Qy	385 ACCAAGACCATCGGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTT	444			
Db	61 ACCAAGACCATCGGACTTTTAAATAAATTTACTCCAAATTTAGCCGAATTTGCTTTTCTT	120			
Qy	445 TGTATAGACAAATAGCTCATCAAAAGTAATTTACTTAACATTTTTTTTAGTCCCTGTTCTA	504			
Db	121 TGTATAGACAAATAGCTCATCAAAAGTAATTTACTTAACATTTTTTTTAGTCCCTGTTCTA	180			
Qy	505 TTGCCACTGCTTTCCCATGTTGAGTTTAGTACTAAAGCCGATACCCATGACGAGATTT	564			
Db	181 TTGCCACTGCTTTCCCATGTTGAGTTTAGTACTAAAGCCGATACCCATGACGAGATTT	240			
Qy	565 TAGAAGGTTTAACTTTTAAATTTGACCGAAATCCAGAGAGCCCAATTCACGAGGTTTTC	624			
Db	241 TAGAAGGTTTAACTTTTAAATTTGACCGAAATCCAGAGAGCCCAATTCACGAGGTTTTC	300			
Qy	625 AAGAGTGTGTGAGAACTTTGAATCAACCTGATTTCAATTTGCAATTAATTAATTAATTA	684			
Db	301 AAGAGTGTGTGAGAACTTTGAATCAACCTGATTTCAATTTGCAATTAATTAATTAATTA	360			
Qy	685 GTTTATTTTGTCTGAAGTTTAAATTTGGTTGACAAATTTCTTGAAGACCTCAAGAAAC	744			

herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.

**Homo sapiens.**

Key	Location/Qualifiers
CDS	1..1182
	/*tag= a
	/product= "Alpha-1-antitrypsin"
	/partial
	/note= "No start or stop codon shown"

WO200250287-A2.

27-JUN-2002.

18-DEC-2001; 2001WO-US49256.

18-DEC-2000; 2000US-3

20-NOV-2001; 2001US-331966P.

(ARRI-) ARRIVA PHARM INC.

Barr PJ, Gibson HL, Pemberton P;

WPI; 2002-500631/53.  
P-DCRB. 22000072

**Notes:**

with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor -

Disclosure: Page 24-25; 134pp; English.

This invention relates to a novel fusion protein comprising a first protease inhibitor comprising an alpha1-antitrypsin or its functionally active portion and a second protease inhibitor or its functionally active portion. The fusion proteins of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, chronic obstructive pulmonary disease, cystic fibrosis, otitis media, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder involving unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and psoriasis, in inflammatory responses to viral infection, and for treating herpes infection, corneal or epidermal ulceration, chronic non-healing wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour angiogenesis, gastric ulceration, osteoporosis, Paget's disease, glomerulonephritis, scleroderma, bacterial infection, Alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the DNA encoding the human alpha-1-antitrypsin (AAT) protein used to create the fusion protein of the invention.

Sequence 1182 BP; 369 A; 214 C; 229 G; 370 T; 0 other;

Query Match	77.5%;	Score 1182;	DB 24;	Length 1182;
Best Local Similarity	100.0%;	Pred. No. 4e-287;		
Matches 1182;	Conservative	0;	Mismatches 0;	Indels 0;
				Gaps 0;

QY 336 GAAGACCTCAAGGCGACGCCGCTCAAAAACCGACACCCAGTCATCAGACCAAGACCAT 395

db

1 GAAGACCCCTCAAGGCGACGCCGCTCAAAAAACCGACACCGTCATCAGCACCCACGCCAT 60

[illegible][illegible][illegible]

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
84

Db	121	TTAGCTCATCAAGTAATCTCTACTAACATTTTTTTTGTAGTCTGTTTCTATTGCCACTGCT	181
Qy	516	TTGCCATGTTGAGTTTGTAGTACTAAAGCCGATACCATGACGAGATTTTGAAGGTTTA	575
Db	181	TTGCCATGTTGAGTTTGTAGTACTAAAGCCGATACCATGACGAGATTTTGAAGGTTTA	240
Qy	576	AACHTTAAHTTGACCGAAATCCCAGAAAGCCCAAAHTTACGAGGGTTTTCAGAGTGTGTG	635
Db	241	AACHTTAAHTTGACCGAAATCCCAGAAAGCCCAAAHTTACGAGGGTTTTCAGAGTGTGTG	300
Qy	636	AGAACTTTGAATCAACCTGATCTCTCAATTGCAAATAACTACTTGTAACGGTTTATTTTGTG	695
Db	301	AGAACTTTGAATCAACCTGATCTCTCAATTGCAAATAACTACTTGTAACGGTTTATTTTGTG	360
Qy	696	TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAAAGCGTCAAGAAACTATATCATAGT	755
Db	361	TCTGAAGGTTTAAATTTGGTTGACAAATTCCTAGAAAGCGTCAAGAAACTATATCATAGT	420
Qy	756	GAGCGTTTTACCGTTAAHTTTGGTGATCTGAGGAGCTTAAAGCCAAATTAATGATTAT	815
Db	421	GAGCGTTTTACCGTTAAHTTTGGTGATCTGAGGAGCTTAAAGCCAAATTAATGATTAT	480
Qy	816	GTTGAGAAAGCCACCCAGGGTAAGATCGTTGACCTAGTTTAAAGAAATAGATCGTGATACC	875
Db	481	GTTGAGAAAGCCACCCAGGGTAAGATCGTTGACCTAGTTTAAAGAAATAGATCGTGATACC	540
Qy	876	GTCTTCGCATAGTTAACTATATTTTTTTCAGGGTGAAGTGGGAACGTCCTTTCAGAGTT	935
Db	541	GTCTTCGCATAGTTAACTATATTTTTTTCAGGGTGAAGTGGGAACGTCCTTTCAGAGTT	600
Qy	936	AAAGATACTCAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCMAAGTTTCCAATG	995
Db	601	AAAGATACTCAAGAGGAAGATTTTCATGTTGATCAAGTTACTACTGTCMAAGTTTCCAATG	660
Qy	996	ATGAAAAGACTGGGTATGTTCAATATTTCAACATTCGCAAAAATTAAGTTCCTTGGGTCTTA	1055
Db	661	ATGAAAAGACTGGGTATGTTCAATATTTCAACATTCGCAAAAATTAAGTTCCTTGGGTCTTA	720
Qy	1056	TTAATGAAGTATTTAGGTAAACGCTACTGCTATTTTTTTTTTACCAGAGCAAGGTAAGCTT	1115
Db	721	TTAATGAAGTATTTAGGTAAACGCTACTGCTATTTTTTTTTTACCAGAGCAAGGTAAGCTT	780
Qy	1116	CAACATTTAGAGAAATGAGTTGACTCATGACATTTATCTAAATTTTGAAGAACGAGAT	1175
Db	781	CAACATTTAGAGAAATGAGTTGACTCATGACATTTATCTAAATTTTGAAGAACGAGAT	840
Qy	1176	CGTCTGAGCGCTTCTCGACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAA	1235
Db	841	CGTCTGAGCGCTTCTCGACCTGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAA	900
Qy	1236	TCGTGTTTTAGGCCAGTTAGGTATTTACCAAGTTTTTTTCTAACGGTCCGGATTTGAGTGGT	1295
Db	901	TCGTGTTTTAGGCCAGTTAGGTATTTACCAAGTTTTTTTCTAACGGTCCGGATTTGAGTGGT	960
Qy	1296	GTTACTGAAGAAGCTCCATTAATAATGAGTAAGCTGTTCAAAAGCGCTCTTAACATT	1355
Db	961	GTTACTGAAGAAGCTCCATTAATAATGAGTAAGCTGTTCAAAAGCGCTCTTAACATT	1020
Qy	1356	GATGAAAAGGTTACCGAGGCCCGCGCGGTATGTTCTCTGGAAGCTATTCCAATGAGCATT	1415
Db	1021	GATGAAAAGGTTACCGAGGCCCGCGCGGTATGTTCTCTGGAAGCTATTCCAATGAGCATT	1080
Qy	1416	CCACCGAAGTTAAATTTAAATAACCATTCGTTTTTCTTGATGATCGAGCAGAACACTAAA	1475
Db	1081	CCACCGAAGTTAAATTTAAATAACCATTCGTTTTTCTTGATGATCGAGCAGAACACTAAA	1140
Qy	1476	AGCCCATGTTATGGGTAAAGTTGTTCAACCCAACTCAGAAG	1517
Db	1141	AGCCCATGTTATGGGTAAAGTTGTTCAACCCAACTCAGAAG	1182
RESULT	8		
AAV411730			

RESULT 8  
AAV41730



QY 1476 AGCCCATGTTTGGTGAAGTTGTCACACCCCAACTCAGAGT 1518  
 DB 1216 AGCCCTCTTTCATGAGGGAAGTGTCTCAACCCCAAGAGT 1258

## RESULT 9

AA089254

ID AAQ89254 standard; cDNA; 1312 BP.

AC AAQ89254;

XX 18-OCT-1995 (first entry)

XX Human alpha-1-trypsin cDNA.

XX Alpha-1-trypsin; protease-inhibitor; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 28..1258

XX sig\_peptide /tag= a

XX mat\_peptide /tag= b

XX US5399684-A.

XX 21-MAR-1995.

XX 20-MAY-1982; 82US-0380310.

XX 20-MAY-1982; 82US-0380310.

XX 07-FEB-1984; 84US-0638980.

XX 03-MAR-1987; 87US-0022543.

XX 15-DEC-1987; 87US-0133190.

XX 16-SEP-1988; 88US-0246912.

XX 22-AUG-1989; 89US-0398288.

XX 11-MAR-1991; 91US-0666450.

XX 18-NOV-1992; 92US-0979556.

XX 02-JUL-1993; 93US-0086442.

XX (WASH-) WASHINGTON RES FOUND.

XX Davie EW, Kurachi K, Thirumalachary C, Woo SLG;

XX WPI; 1995-130740/17.

XX P-PSDB; AAR71969.

XX Human alpha-1-trypsin (al-AT) cDNA sequence - can be used for

XX the expression of al-AT

XX Claim 1; Fig.1; 15pp; English.

XX The sequence of a human alpha-1-antitrypsin cDNA clone is given in

XX CC AAQ89254. Expression of the cDNA in host cell transformants has

XX CC allowed production of recombinant alpha-1-antitrypsin.

XX SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;

XX Query Match 28.6%; Score 436.4; DB 16; Length 1312;

XX Best Local Similarity 59.8%; Pred. No. 1.1e-99;

XX Matches 731; Conservative 0; Mismatches 491; Indels 0; Gaps 0;

QY 298 TGTGTGGTAAAGTCCTGTTTCCCAGTCAAGGCCATGAAGACCCCTCAAGCGCAGCGC 357

DB 62 TGGCAGGCCCTGTGCTGCCGTGGTCCCTGTCTCCCTGGCTGAGGATCCCCAGGAGATGCTG 121

QY 358 CTCACAAAACCCAGCAGTGTATCAGGACCAAGACATCCGACTTTTAAATAAATATCTC 417

DB 122 CCAGAGACAGATACATCCCACCATGATCAGGATCACCCACCTTCAACAGATCACCC 181

QY 418 CAAATTTAGCCGAAATTTCTTTTCTTTGTATAGACAATAGCTCATCAAAAGTAATCTA 477  
 DB 182 CCAACTTGGCTGAGTTTCGCTTACGCTTATACCGCCAGCTGGCACACCAAGTCCAACAGCA 241  
 QY 478 CTAACATTTTGTAGTCTCTGTTTCTATGTCACCTGCTTCCGCTATGTTAGTGTAGGTA 537  
 DB 242 CCAATATCTTCTTCCCCAGTGGAGCATCGCTACAGCCTTTGCAATGCTCTCCCTGGGGA 301  
 QY 538 CTAAAGCCGATACCCATGACGAGATTTTGAAGAGTTTAAACTTTAAATTTGACCGAAATCC 597  
 DB 302 CCAAGGCTGACACTCACGATGAATCTCGAGGGCTCAATTTCAACTCAGGAGATTC 361  
 QY 598 CAGAAAGCCCAATTCACGAGGGTTTTCAAGAGTTGTTGAGAACTTTGAATCAACTGATT 657  
 DB 362 CGGAGGCTCAGATCCATGAAGGCTTCCAGAACTCTCCGTACCTCAACAGCCAGACA 421  
 QY 658 CTCATTTGCAATTAACCTACTGTAACGGTTTATTTTGTCTGAAGGTTTAAATTTGGTTG 717  
 DB 422 GCCAGCTCCAGCTGACCAACCGCAATGSCCTGTCTCAGCGAGGGCTGAAGCTAGTGG 481  
 QY 718 ACAAATTCCTAGAAGACGCTCAAGAACTATATCATGAGGCTTTTACCGTTAATTTTG 777  
 DB 482 ATAAGTTTTTGAGGATGTTTAAAGTTGTACCACTCAGAAAGCTTCACTGTCAACTTCG 541  
 QY 778 GTGATACTGAGAAAGCTAAAAGCAAAATTAATGATTATGTTGAGAAAGCCAGGGTA 837  
 DB 542 GGGACCCGAAAGAGGCCAAGAAACAGATCAACGATTACGTGAGAGGGGTACTCAAGGGA 601  
 QY 838 AGATCGTTGACCTAGTTTAAAGAATTAGATCGTATACGCTCTCCGACTAGTTAACTATA 897  
 DB 602 AAATTTGGATTTGGTCAAGGAGCTTGACAGAGACACAGTTTTTGTCTGTGTGAATTACA 661  
 QY 898 TTTTTCGAAGGGTAAGTGGGAACGTCCTTTTCGAGGTTTAAAGTACTCAAGAGGAAGATT 957  
 DB 662 TCTTCTTTAAAGGCAATGGGAGAGACCCCTTTGAAGTCAAGGACACCGAGGAGGACT 721  
 QY 958 TTCATGTTGATCAAGTTACTACTGTCRAAGTTCCTCAAGTATGATCAAGAAAGCTGGGTATGTCA 1017  
 DB 722 TCCAGGTGGACCGAGTGACCACTGAGGTCCTATGATGAAGCGTTTAGGCATGTTTA 781  
 QY 1018 ATATTCAACATTTGCAAAAATTAAGTTCTTGGGCTTTATTAATGAAGTATTTAGGTAAAG 1077  
 DB 782 ACATCCAGCATTTGAAGAAGCTGTCCAGCTGGGTGCTGCTGATGAATACCTGGGCAATG 841  
 QY 1078 CTACTGCTATTTTTTTTACCAGAGAGTAAAGCTTCAACATTTAGAAATGAGTGTGA 1137  
 DB 842 CCACCGCCATCTTCTTCTGCTGATGAGGGGAACTACAGCACTGGAATGAACATCA 901  
 QY 1138 CTCATGACATTTACTAAATTTTGTAGAGAACGAGGATCGTCGTAGCGCTTCTCTGCACC 1197  
 DB 902 CCCAGGATATCATCCCAAGTCTCTGGAAATGAGACAGAAAGTCTGCCAGCTTAGATT 961  
 QY 1198 TGCCAAAGTTAAGTATCACCCGTTACTTACGACTTTAAATCTGTTTTAGGCGAGTTAGGTA 1257  
 DB 962 TACCCAAACTGCTCCATTTACTGGAACCTATGATCTGAAGAGGCTCTTAGGTCAACTGGCA 1021  
 QY 1258 TTACCAAGTTTTTTTCTAACGGTCCGATTTGAGTGGTGTGTTTACTGAAGAGCTCCATTA 1317  
 DB 1022 TCACCTAAGGCTTTCAGCAATGGGCTGACCTCTCCGGGGTCCACAGAGAGGAGCCCTCGA 1081  
 QY 1318 AATTGAGTAAAGCTGTTTCAACAAAGCCGCTTAACTATTTGATGAAGAGGTTACCGAGCCG 1377  
 DB 1082 AGCTCTCAAGCCGCTGCATGAGCTGTGTGACCATCGAGGAGAAAGGACTGAAGCTG 1141  
 QY 1378 CCGGCGCTATGTTCTGGAAGCTATTCCCAATGAGCATTTCCACCAAGAGTTTAAATTTAATA 1437  
 DB 1142 CTGGGGCCATGTTTTTAGAGGCCATACCATGCTATCCGCCCGCCGAGGTCAAGTTCACA 1201  
 QY 1438 AACCATTCGTTTTTCTGATGATCAGGAGAACACTAAAGCCCATTTTATGGGTAAAG 1497  
 DB 1202 AACCTTTGTCTTCTTAATGATTGAACAAATAACCAAGTCTCCCTCTCTTCATGGGAAAG 1261



Db 1262 TGGTGAATCCCAACCAATA 1283  
 RESULT 11  
 AA290199  
 ID AA290199 standard; cDNA; 1312 BP.  
 XX  
 AC AA290199;  
 XX  
 DT 19-MAY-2000 (first entry)  
 XX  
 DE Human alpha1-antitrypsin nucleotide sequence.  
 XX  
 KW Alpha1-antitrypsin; neutrophil elastase inhibitor; human; ss;  
 KW chronic obstructive pulmonary emphysema; infantile liver cirrhosis.  
 OS Homo sapiens.  
 XX  
 PN US6025161-A.  
 XX  
 PD 15-FEB-2000.  
 XX  
 PF 20-JAN-1998; 98US-0009581.  
 XX  
 PR 07-JUN-1995; 95US-0479545.  
 PR 20-MAY-1982; 82US-0380810.  
 PR 07-FEB-1984; 84US-0638980.  
 PR 03-MAR-1987; 87US-0022543.  
 PR 15-DEC-1987; 87US-0133190.  
 PR 16-SEP-1988; 88US-0246912.  
 PR 22-AUG-1989; 89US-0398288.  
 PR 11-MAR-1991; 91US-0666450.  
 PR 18-NOV-1992; 92US-0879556.  
 PR 02-JUL-1993; 93US-0086442.  
 XX  
 PA (WASH-) WASHINGTON RES FOUND.  
 XX  
 PI Woo SLC, Thirumalachary C, Kurachi K, Davie EW;  
 XX  
 DR WPI: 2000-181811/16.  
 DR P-PSDB: AAY78890.  
 XX  
 PT Preparing alpha1-antitrypsin for inhibiting neutrophil elastase  
 PT involves transfected host cell with vector comprising  
 PT alpha1-antitrypsin DNA sequence that hybridizes to human  
 PT alpha1-antitrypsin cDNA, or its complement -  
 XX  
 PS Claim 1; Fig 1; 16pp; English.  
 XX  
 CC This sequence represents the human alpha1-antitrypsin nucleotide  
 CC sequence. Alpha1-antitrypsin is an important protease inhibitor, the  
 CC major function of which is to inhibit neutrophil elastase. Low levels of  
 CC alpha1-antitrypsin in the blood are associated with chronic obstructive  
 CC pulmonary emphysema and infantile liver cirrhosis. A vector comprising a  
 CC mammalian alpha1-antitrypsin DNA sequence that hybridizes to human  
 CC alpha1-antitrypsin cDNA can be introduced into a host cell in a method  
 CC for the production of alpha1-antitrypsin.  
 XX  
 SQ Sequence 1312 BP; 339 A; 368 C; 324 G; 281 T; 0 other;  
 Query Match 28.6%; Score 436.4; DB 21; Length 1312;  
 Best Local Similarity 59.8%; Pred. No. 1.1e-99;  
 Matches 731; Conservative 0; Mismatches 491; Indels 0; Gaps 0;  
 QY 298 TGTGTGTAAGTCTGTGTTCCCAAGTCAAGCCATGAAGACCCCTCAAGGCGGCGG 357  
 Db 62 TGCAGGCTGTGCTGGTCCCTGTCTCCCTGGCTGAGGATCCCAAGGAGATGCTG 121  
 QY 358 CTCAAAAACCGACACGAGTCATCAGCAGCAAGACCATCCGACTTTTAATAAATTAATC 417  
 Db 122 CCCAGAAGACAGATATATCCCAAGTATCAGATCACCACCTTCAACAAGATCACCC 181

QY 418 CAAATTTAGCCGAATTTGCTTTTCTTTGTATAGACAATTTAGCTCATCAAGTAATTTCTA 477  
 Db 182 CCAACTTGGCTGAGTTCGCCCTTACGCCATATACGCCAGCTGGCACACCATCTCAACAGCA 241  
 QY 478 CTAACATTTTTTTTAGTCTGTTTCTATGCCACTGCTTTGCCCATGTTGAGTTTAGGTA 537  
 Db 242 CCAATATCTTTCTTCTCCCAAGTACGATCGCTACAGCCTTTGCAATGCTCTCCCTGGGA 301  
 QY 538 CTAAGCCGATACCCATGACGAGATTTTACAAGGTTTAACTTTTAACTTTGACCGAATCC 597  
 Db 302 CCAAGGCTGACACTCAGATGAATCTGGAGGCGCTGAATTTCAACCTCACGGAGATTC 361  
 QY 598 CAGAAGCCCAATTCACGAGGTTTCAAGAGTTTGTGAGAACTTTGAAATCAACCTGATTC 657  
 Db 362 CGGAGGCTCAGATCCATGAAGGTTCCAGCAACTCTCCGTACCTCAACCCAGCAGACA 421  
 QY 658 CTCAATTCGAATTAACCTACTGTTAAGGTTTATTTTGTCTGAAGTTTAAATTTGGTTG 717  
 Db 422 GCCAGCTCCAGCTGACCGCCGCAATGGGCTGTTCTCAGCAGGCGCTGAGCTAGTGG 481  
 QY 718 ACAATTTCTTAGAAGACGTCAGAAACTATATCATAGTGAGGCTTTTACCGTTAATTTTG 777  
 Db 482 ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTCACTGCTCAACTCG 541  
 QY 778 GTGATCTAGGAGGCTAAAAAGCAAAATTAATGATTATGTTGAGAAAGGCACCCAGGTA 837  
 Db 542 GGGACACCGAAGAGGCCAAGAAACAGATCAACGATTACGTGGAGAGGGTACTCAAGGGA 601  
 QY 838 AGATCGTTGACCTAGTTAAGAAATTAAGATAGCTGATACCGTCTTCGCACACTAGTTAATA 897  
 Db 602 AATTTGTGATTTGGTCAAGGAGCTTTGACAGAGACACAGTTTGTCTGTTGTAATTA 661  
 QY 898 TTTTTCGAAGGTAAGTGGGAACGCTCTTTCGAGGTTTAAAGATACTGAAGAGGAGATTC 957  
 Db 662 TCTTCTTTAAGGCAATGGGAGAGACCTTTGAAGTCAAGGACCCGAGGAGGAGGACT 721  
 QY 958 TTCATGTTGATCAAGTTACTACTGTCAAAGTTCCTCAATGATGAAAAGACTGGGTATGTTCA 1017  
 Db 722 TCCACGTGGACCAAGGTGACCCCGTGAAGGTGCTATGATGAAGCGTTTGAAGCATGTTTA 781  
 QY 1018 ATATTCACATTTGCAAAAAATTAAGTTCTTGGTCTCTTATTAATGAAGTATTTAGTAAAG 1077  
 Db 782 ACATCCAGCATTTGTAAGAAGCTGTCCAGCTGGGTGCTGCTGATGAATACCTTGGGCAATG 841  
 QY 1078 CTATGCTATTTTTTTTACCAGAGCAAGGTAAGCTTCAACATTTAGAGAATGAGTTGA 1137  
 Db 842 CCACCGCCATCTTCTCCTGCTGATGAGGGGAAACTACAGCACCTGGAAATGAATCA 901  
 QY 1138 CTCATGACATTTATTACTAATTTTGTAGAGACGAGATCGTACGCGTCTCTGACACC 1197  
 Db 902 CCCAGATATCATCAACCAAGTTCTTGGAAATGAAGACAGAGAGTCTGCCAGCTTACATTC 961  
 QY 1198 TGCCAAAGTTAAGTATCACCGGTACTTACGACTTAAATCTGTTTTTAGCCAGTTAGGTA 1257  
 Db 962 TACCACAACTGTCATTTACTGAACTATGATCTCAAGAGCGTCTAGTCACTGAGTGGGA 1021  
 QY 1258 TTACCAAGTTTTTTTCTAACGCTGCCGATTTGAGTGGTGTACTGAAGAAGCTCCATTAA 1317  
 Db 1022 TCACCTAAGGTCTTTCAGCAATGGGCTGACCTCTCCGGGTGCACAGAGGAGCACCCCTGA 1081  
 QY 1318 AATTGAGTAAAGCTGTTCAAGGCGCTTAACTATTTGATGAAGAGGTACCGAGGCGG 1377  
 Db 1082 AGCTCTCAAGGCGCTGATAGGCTGTGCTGACCATCGACGAGAAAGGAGTGAAGCTG 1141  
 QY 1378 CGGCGCTATGTTCTTGGAAAGCTATTCCAATGAGCATTTCCACCAAGAGTTTAAATTTAATA 1437  
 Db 1142 CTGGGGCCATGTTTTTACAGGCCATACCCATGCTATCCGCGCCGAGGCTCAAGTTCACA 1201  
 QY 1438 ACCATTCGTTTTTCTGATGATCGAGCAGACACTTAAAGCCCCATTTGTTATGGTAAAG 1497  
 Db 1202 AACCTTTGCTTCTTAATGATGAACAAAAATACCAAGTCTCCCTCTCTTCATGGGAAAG 1261  
 QY 1498 TTGTCAACCCCAACTCAGAAGTA 1519





Db 894 CCACGATATCATCACCAAGTCTCTGGAAAAATGAAGACAGAAAGGTCTGCCAGCTTACATT 953  
 QY 1198 TGGCAAGTTAAGTATACACGGTACTTACGACTTAAATCTGTTTATAGCCAGTTAGGTA 1257  
 Db 954 TACCCAACTGTCCATTACTTGAACCTATGATCTGAAGAGCGTCTGGGTCAACTGGGCA 1013  
 QY 1258 TTACCAAGTTTCTTAACCGTGGCGATTGAGTGTGTACTGAAGAAGCTTCCATTAA 1317  
 Db 1014 TCATAAGGCTTTCAGCAATGGGGCTGACCTCTCCGGGTTCAGAGGAGGACCCCTGA 1073  
 QY 1318 AATTGAGTAAAGCTGTTTCACAAAGCGGTCTTAATCTATGATGAAAAGGTACCGAGCGG 1377  
 Db 1074 AGCTCTCAAGGCGTGCATAAGGCTGTGCTGACCATCGAGAGAAAGGACTGAAGCTG 1133  
 QY 1378 CCGGCGTATGTTCTCGAAGCTATTCCATGAGCATTCACACAGAAAGTTAAATTTAAATA 1437  
 Db 1134 CTGGGGCATGTTTTTATAGAGCCCATACCATGCTATCCCGGCTGAGGTCAGTTCAACA 1193  
 QY 1438 AACCATTCGTTTTTCTGATGATGAGCAGACACTAAAGCCCATTTGTTATGGGTAAGG 1497  
 Db 1194 AACCTTTGCTTCTTATGATTAACAAATAACCAAGTCTCCCGCTCTTCATGGGAAAG 1253  
 QY 1498 TTGTCAACCCCAACTCAGAATGA 1519  
 Db 1254 TGGTGAATCCCAACCAATAATA 1275

RESULT 14  
 ID ABL67511 standard; DNA; 1352 BP.  
 AC ABL67511;  
 XX  
 DT 15-MAY-2002 (first entry)  
 DE Thyroid cancer related gene sequence SEQ ID NO:5848.  
 KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
 KW cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;  
 KW gene; ds.  
 OS Homo sapiens.  
 XX  
 PN WO200194629-A2.  
 XX  
 PD 13-DEC-2001.  
 XX  
 PF 30-MAY-2001; 2001WO-US10838.  
 XX  
 PR 05-JUN-2000; 2000US-209473P.  
 PR 05-JUN-2000; 2000US-209531P.  
 PR 18-SEP-2000; 2000US-233133P.  
 PR 18-SEP-2000; 2000US-233617P.  
 PR 20-SEP-2000; 2000US-234009P.  
 PR 20-SEP-2000; 2000US-234034P.  
 PR 20-SEP-2000; 2000US-234052P.  
 PR 22-SEP-2000; 2000US-234509P.  
 PR 22-SEP-2000; 2000US-234567P.  
 PR 25-SEP-2000; 2000US-234923P.  
 PR 25-SEP-2000; 2000US-234924P.  
 PR 25-SEP-2000; 2000US-235077P.  
 PR 25-SEP-2000; 2000US-235082P.  
 PR 25-SEP-2000; 2000US-235134P.  
 PR 25-SEP-2000; 2000US-235280P.  
 PR 26-SEP-2000; 2000US-235637P.  
 PR 26-SEP-2000; 2000US-235638P.  
 PR 27-SEP-2000; 2000US-235711P.  
 PR 27-SEP-2000; 2000US-235720P.  
 PR 27-SEP-2000; 2000US-235840P.  
 PR 27-SEP-2000; 2000US-235863P.  
 PR 28-SEP-2000; 2000US-236028P.  
 PR 28-SEP-2000; 2000US-236032P.

PR 28-SEP-2000; 2000US-236033P.  
 PR 28-SEP-2000; 2000US-236034P.  
 PR 28-SEP-2000; 2000US-236109P.  
 PR 28-SEP-2000; 2000US-236111P.  
 PR 29-SEP-2000; 2000US-236842P.  
 PR 29-SEP-2000; 2000US-236891P.  
 PR 02-OCT-2000; 2000US-237172P.  
 PR 02-OCT-2000; 2000US-237173P.  
 PR 02-OCT-2000; 2000US-237278P.  
 PR 02-OCT-2000; 2000US-237294P.  
 PR 02-OCT-2000; 2000US-237295P.  
 PR 02-OCT-2000; 2000US-237316P.  
 PR 03-OCT-2000; 2000US-237425P.  
 PR 03-OCT-2000; 2000US-237598P.  
 PR 03-OCT-2000; 2000US-237604P.  
 PR 03-OCT-2000; 2000US-237606P.  
 PR 03-OCT-2000; 2000US-237608P.  
 PR 01-NOV-2000; 2000US-244867P.  
 PR 01-NOV-2000; 2000US-245084P.  
 PA (AVAL-) AVALON PHARM.  
 XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
 PI Soppet DR, Weaver Z;  
 XX WPI; 2002-188264/24.  
 XX  
 PT Screening for anti-neoplastic agent involves exposing cells to a  
 PT chemical agent to be tested for anti-neoplastic activity, and  
 PT determining a change in expression of a gene of a signature gene set  
 XX  
 PS Claim 1; SEQ ID 5848; 44pp; English.  
 XX  
 CC The present invention describes a method (M1) for screening for an  
 CC anti-neoplastic agent. The method involves exposing cells to a chemical  
 CC agent to be tested for anti-neoplastic activity, determining a change in  
 CC expression of at least one gene (I) of a signature gene set, where (I)  
 CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
 CC to ABL70110), or is at least 95% identical to (S), where a change in  
 CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
 CC activity and can be used in gene therapy. M1 can be used for screening  
 CC an anti-neoplastic agent, and can be used for producing a product which  
 CC is the data collected with respect to the anti-neoplastic agent as a  
 CC result of M1, and the data is sufficient to convey the chemical  
 CC structure and/or properties of the agent. M1 can be used in the  
 CC treatment of cancer such as colon, breast, stomach, lung, thyroid,  
 CC oesophageal, ovarian, kidney, prostate or pancreatic cancer,  
 CC adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer,  
 CC infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine  
 CC carcinoma, papillary carcinoma and Wilms' tumour.  
 XX  
 SQ Sequence 1352 BP; 349 A; 386 C; 325 G; 292 T; 0 other;

Query Match 28.4%; Score 433.2; DB 24; Length 1352;  
 Best Local Similarity 59.7%; Pred. No. 6.8e-99;  
 Matches 729; Conservative 0; Mismatches 493; Indels 0; Gaps 0;

QY 298 TGTGTGTAAGTCTGTTTCCCGAGTCAAGGCATGGAAGACCCCTCAAGGGGACGCCG 357  
 Db 54 TGGCAGGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 113  
 QY 358 CTCAAAAACCGACACAGTATCATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 417  
 Db 114 CCCAGAGACAGATACATCCACCATGATCAGGATCAGGATCAGGATCAGGATCAGGAT 173  
 QY 418 CAAATTTAGCCGAATTTGCTTTTCTTTGATAGACAAATAGCTCATCAAGTAATCTA 477  
 Db 174 CCAACCTGGCTGAGTTCCGCTTATACCGCCTATACCGCAGCTGGCACACAGTCCACAGCA 233  
 QY 478 CTACATATTTTGTAGTCTGCTTTCTATTGCGCACTGCTTTCGCAATGTTGAGTTAGTA 537  
 Db 234 CCAATATCTTCTTCTCCCGCAGTGAGCATCGCTACAGCCTTTTGCATGCTCTCCCTGGGGA 293



